ABSTRACT

Disclosed is a computational method for predicting intramolecular and intermolecular biopolymer interactions which provides an improved way of determining structure and function information, including intramolecular and intermolecular interactions using an *ab initio*-type approach, i.e. using only sequence information. The method is a widely applicable sequence-mining tool capable of detecting both intramolecular and intermolecular interactions for all biopolymers, including, but not limited to, DNA, RNA and protein. It possesses an adaptive screening process that allows for high accuracy. It can be an entirely rule-free, unbiased methodology, and thus can detect novel interactions for all biopolymers. Due to the incorporation of a misalignment process, it can be used iteratively and is capable of refining its own predictions and detecting and managing errors. Therefore, the disclosed method also provides a technique for more accurately determining (and refining) sequence alignments.